```
      10                  30                  50
TCCTGCGTTATCCCCCTGATTCTGTGGATAACCGTATTNCCGCCTTTGAGTGAGCTGATA
      70                  90                  110
CCGCTCNCCNCAGCCGAACGACCGAGCGCAGCGAGTCAGTGAGCGAGGAAGCGGAAGAGC
      130                 150                 170
GCCCAATACGCAAACCGCCTCTCCCCGCGCGTTGGCCGATTCATTAATGCAGCTGGCACG
      190                 210                 230
ACAGGTTTCCCGACTGGAAAGCGGGCAGTGAGCGCAACGCAATTAATGTGAGTTAGCTCA
      250                 270                 290
CTCATTAGGCACCCCAGGCTTTACACTTTATGCTTCCGGCTCGTATGTTGTGTGGAATTG
      310                 330                 350
TGAGCGGATAACAATTTCACACAGGAAACAGCTATGACCATGATTACGCCAAGCTCGAAA
      370                 390                 410
TTAACCCTCACTAAAGGGAACAAAAGCTGGAGCTCCACCGCGGTGGCGNCCGCTCTAGAA
      430                 450                 470
CTAGTGGATCCCCCGGNCTGCAGGGGCACACACACGCACACATACACAGAATCCTCAGAT
      490                 510                 530
AACAGGAGGCAATAAATCCAACAGCACATCCACGTTCAGAGAACAGTGTCCCTGCTGTCT
      550                 570                 990
TGCTAACAGCTGCCAATACCTCACTGAGTGCCTCACACCAACATGGGCTCCAAGTGAGTT
      610                 630                 650
TCATTCGTCTGGGCAGACTCCCTCCCCTCTTCCATAAAGGCTGCAGGAGACCTGTAGCTG
      670                 690                 710
TCACAGGACCTTCCCTAAGAGCCCGCAGGGGGAAGACTGCCCCAGTCCGGCCATCACCAT
                                                              M
      730                 750                 770
GCTCCGGCCCATTCTGGATGCTCCCCAGCGGTTGCTGAAGGAGGGGAGAGCGTCCCGGCA
 L  R  P  I  L  D  A  P  Q  R  L  L  K  E  G  R  A  S  R  Q
      790                 810                 830
```

FIG.1A

```
GCTGGTGCTGGTGGTGGTATTCGTCGCTTTGCTCCTGGACAACATGCTGTTTACTGTGGT
 L  V  L  V  V  V  F  V  A  L  L  L  D  N  M  L  F  T  V  V
       850                 870                 890
GGTGCCAATTGTGCCCACCTTCCTATATGACATGGAGTTCAAAGAAGTCATCTCTTCTCT
 V  P  I  V  P  T  F  L  Y  D  M  E  F  K  E  V  I  S  S  L
       910                 930                 950
GCACCTCGGGCATGCCGGAAGTTCCCCACATGCCCTCGCCTCTCCTGCCTTTTCCACCAT
 H  L  G  H  A  G  S  S  P  H  A  L  A  S  P  A  F  S  T  L
       970                 990                1010
CTTCTCCTTCTTCAACAACAACACCGTGGCTGTTGAAGAAAGCGTACCTAGTGGAATAGC
 F  S  F  F  N  N  N  T  V  A  V  E  E  S  V  P  S  G  I  A
      1030                1050                1070
ATGGATGAATGACACTGCCAGCACCATCCCACCTCCAGCCACTGAAGCCATCTCAGCTCA
 W  M  N  D  T  A  S  T  I  P  P  P  A  T  E  A  I  S  A  H
      1090                1130                1130
TAAAAACAACTGCTTGCAAGGCACAGGTTTCTTGGAGGAAGAGACTACCCGGGTCGGGGT
 K  N  N  C  L  Q  G  T  G  F  L  E  E  E  T  T  R  V  G  V
      1150                1170                1190
TCTGTTTGCTTCAAAGGCTGTGATGCAACTTCTGGTCAACCCATTCGTGGGCCCTCTCAC
 L  F  A  S  K  A  V  M  Q  L  L  V  N  P  F  V  G  P  L  T
      1210                1230                1250
CAACAGGATTGGATATCATATCCCCATGTTTGCTGGCTTTGTTATCATGTTTCTCTCCAC
 N  R  I  G  Y  H  I  P  M  F  A  G  F  V  I  M  F  L  S  T
      1270                1290                1310
AGTTATGTTTGCTTTTTCTGGGACCTATACTCTACTCTTTGTGGCCCGAACCCTTCAAGG
 V  M  F  A  F  S  G  T  Y  T  L  L  F  V  A  R  T  L  Q  G
      1330                1350                1370
```

FIG.1B

```
CATTGGATCTTCATTTTCATCTGTTGCAGGTCTTGGAATGCTGGCCAGTGTCTACACTGA
 I  G  S  S  F  S  S  V  A  G  L  G  M  L  A  S  V  Y  T  D
      1390                1410                1430
TGACCATGAGAGAGGACGAGCCATGGGAACTGCTCTGGGGGGCCTGGCCTTGGGGTTGCT
 D  H  E  R  G  R  A  M  G  T  A  L  G  G  L  A  L  G  L  L
      1450                1470                1490
GGTGGGAGCTCCCTTTGGAAGTGTAATGTACGAGTTTGTTGGGAAGTCTGCACCCTTCCT
 V  G  A  P  F  G  S  V  M  Y  E  F  V  G  K  S  A  P  F  L
      1510                1530                1550
CATCCTGGCCTTCCTGGCACTACTGGATGGAGCACTCCAGCTTTGCATCCTACAGCCTTC
 I  L  A  F  L  A  L  L  D  G  A  L  Q  L  C  I  L  Q  P  S
      1570                1590                1610
CAAAGTCTCTCCTGAGAGTGCCAAGGGGACTCCCCTCTTTATGCTTCTCAAAGACCCTTA
 K  V  S  P  E  S  A  K  G  T  P  L  F  M  L  L  K  D  P  Y
      1630                1650                1670
CATCCTGGTGGCTGCAGGGTCCATCTGCTTTGCCAACATGGGGGTGGCCATCCTGGAGCC
 I  L  V  A  A  G  S  I  C  F  A  N  M  G  V  A  I  L  E  P
      1690                1710                1730
CACACTGCCCATCTGGATGATGCAGACCATGTGCTCCCCCAAGTGGCAGCTGGGTCTAGC
 T  L  P  I  W  M  M  Q  T  M  C  S  P  K  W  Q  L  G  L  A
      1750                1770                1790
TTTCTTGCCTGCCAGTGTGTCCTACCTCATTGGCACCAACCTCTTTGGTGTGTTGGCCAA
 F  L  P  A  S  V  S  Y  L  I  G  T  N  L  F  G  V  L  A  N
      1810                1830                1850
CAAGATGGGTCGGTGGCTGTGTTCCCTAATCGGGATGCTGGTAGTAGGTACCAGCTTGCT
 K  M  G  R  W  L  C  S  L  I  G  M  L  V  V  G  T  S  L  L
      1870                1890                1910
CTGTGTTCCTCTGGCTCACAAAAATTTTGGTCTCATTGGCCCCAATGCAGGGCTTGGCCT
```

FIG.1C

```
 C  V  P  L  A  H  K  N  F  G  L  I  G  P  N  A  G  L  G  L
      1930                 1950                 1970
TNCCATAGGCATGGTGGAATCTTCTATGATGCCCATCATGGGGCACCTGGTGGATCCACG
 X  I  G  M  V  E  S  S  M  M  P  I  M  G  H  L  V  D  P  R
      1990          2010                 2030
CCACACCTCGGTGTATGGGAGTGTCCACGCCATCGCTGATGTGGCTTTTTGCATGGGCTT
 H  T  S  V  Y  G  S  V  H  A  I  A  D  V  A  F  C  M  G  F
      2050                 2070                 2090
TGCTATAGGCTATTCTGAGTCAGGACTGCCCCATGGAGACCCGGATGTATCAACCCAGAA
 A  I  G  Y  S  E  S  G  L  P  H  G  Q  P  D  V  S  T  Q  K
      2110                 2130                 2150
ACCTCTTCCCTGGACCAGTCACCATGGCTGACCCACGGCTCAGTGGCCTCAAAACCTCTG
 P  L  P  W  T  S  H  H  G  *
      2170                 2190                 2210
 CCTGGGATCTTCTTCCTCCCCTCCCATGGACACTGTCCCTGATACTCTTCTCACCTGTGT
      2230                 2250                 2270
AACTTGTAGCTCTTCMTCTATGCCTTGGTGCCGCAGTGGCCCATCTTTTATGGGAAGACA
      2290                 2310                 2330
GAGTGATGCACCYYCCCGCTGCTGTGAGGTTGATTAAACTTGAGCTGTGACGGGGTTCTG
      2350                 2370                 2390
CAAGGGGTGACTCATTGYATAGAGGTGGTAGTGAGTAATGTGCCCCTGAAACCAGTGGGG
      2410                 2430                 2450
TGACTGACAAGCCTCTTTAATCTGTTGCCTGATTTTCTCTGGCATAGCCCCAACAGATCG
      2470                 2490                 2510
GAAGAGTGTTACCCTCTTTWCCCTCAACGTGTTCTTTCCCGGGTTTTCCCCAGCCGAGTT
```

FIG.1D

2530 2550 2570
GAGAAAATGTTCTCAGCATTGTCTTGCTGCCAAATGCCAGCKTGAAGAGTTWGGTATGKT
2590 2610 2630
TTTTCTNCCATTTATTTTATTTATTWACTAAAGTGAATGATTTTACTGTGGYTAAATCTA
2650 2670 2690
GAGCTGCTAAAAGGGCTTTACCCTCAGTGAAAAGTGTCTTCTATTTNCATWATCTTTCAG
2710 2730 2750
AAACWGGAGCCCATTTCTCTTCTGGTGGAGTTATNGACATCCTCCTGACCNCCCCTGTGT
2770 2790 2810
NTNCCTACCTNTACTGAACCTCTTAGACTCTNAGAAATAAAAGTAGAAGAAAGACAGAAA
2830 2850 2870
AATTAACTGATTAGACCCAAGATTTCATGGAAGAAGTTAAAAGAAACTGCCTTGGAAAT

CCCTC

FIG.1E

Homology Alignment between HATBG78 and
the Rat Amine Transporter

```
  1 MLRPILDAPQRLLKEGRASRQLVLVVVFVALLLDMMFTVVVPIVPTFLY  50
    ||..:|:||||||||||.||.|||||||||||||:||||||||||||
  1 MQVVTGAPQRLLKEGRQSRKLVLVVVFVALLLDNMLLTVVVPIVPTFLY  50

 51 DMEFKEVISSLHLGHAGSSPHALASPAFSTIFSFFNNNTVAVEESVPSGI 100
    . |||:  |||| |...||.:::||.|||||||||:|.|..||| ||  .
 51 ATEFKDSNSSLHRGPSVSSQQALTSPAFSTIFSFFONTTTTVEEHVPFRV 100

101 AWMNDTASTIPPPATEAISAHKNNCLQGTGFLEEETTRVGVLFASKAVMQ 150
    .|   |.:|||||.||| |..|||||||.:|||||..|:|:|||||||||
101 TW...TNGTIPPPVTEASSVPKNNCLQGIEFLEEENVRIGILFASKALMQ 147

151 LLVNPFVGPLTNRIGYHIPMFAGFVIMFLSTVMFAFSGTYTLLFVARTLQ 200
    ||||||||||||||||||||.||:||||||:||||||||.|||||||||
148 LLVNPFVGPLTNRIGYHIPMFVGFMIMFLSTLMFAFSGTYALLFVARTLQ 197

201 GIGSSFSSVAGLGMLASVYTDDHERGRAMGTALGGLALGLLVGAPFGSVM 250
    ||||||||||||||||||:.|||||||.|||||||||||||||||||||
198 GIGSSFSSVAGLGMLASVYTDNYERGRAMGIALGGLALGLLVGAPFGSVM 247
```

FIG.2A

```
 251 YEFVGKSAPFLILAFLALLDGALQLCILQPSKVSPESAKGTPLFMLLKDP 300
     |||||||.|||||||||||||||||||| |||||||||.||.|: ||||
 248 YEFVGKSSPFLILAFLALLDGALQLCILWPSKVSPESAMGTSLLTLLKDP 297

 301 YILVAAGSICFANMGVAILEPTLPIWMMQTMCSPKWQLGLAFLPASVSYL 350
     ||||||||||:|||||||||||||||||||||.||||||||||.||
 298 YILVAAGSICLANMGVAILEPTLPIWMMQTMCSPEWQLGLAFLPASVAYL 347

 351 IGTNLFGVLANKMGRWLCSLIGMLVVGTSLLCVPLAHKNFGLTGPNAGLG 400
     |||||||||||||||||||:||:.||.|||||||||. ||||||||||
348 IGTNLFGVLANKMGRWLCSLVGMVAVGISLLCVPLAHNIFGLIGPNAGLG 397

401 LXIGMVESSMMPIMGHLVDPRHTSVYGSVHAIADVAFCMGFAIGYSESGL 450
    : ||||:||:|||||.||| |||||||||.|||||||:||||| |.:|:
398 FAIGMVDSSLMPIMGYLVDLRHTSVYGSVYAIADVAFCVGFAIGPSTGGV 447

451 PHGDPDVSTQKPLPWTSH 468
      .  :..  ..:  | :
448 IVQVIGFPWLMVIIGTIN 465
```

FIG.2B